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Claims

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1. An amino acid sequence that is a mutant of an enzyme selected from the group consisting of leucine dehydrogenase sequences as described in SEQ ID 2, formate dehydrogenase sequence as described in SEQ ID 1, galactose oxidase sequences as described in SEQ ID 3, and substantial equivalents thereof, wherein:

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when the amino acid sequence is a mutant of a leucine dehydrogenase sequence as described in SEQ ID 2 or a substantial equivalent thereof, the amino acid sequence contains at least one mutation selected from the group consisting of F102S, V33A, S351T, N145S and like mutations in subsantially equivalent sequences;

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when the amino acid sequence is a mutant of a formate dehydrogenase sequence as described in SEQ ID 1 or a substantial equivalent thereof, the amino acid sequence contains at least one mutation selected from the group consisting of D195S, Y196H, K356T and like mutations in subsantially equivalent sequences; and

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when the amino acid sequence is a mutant of a galactose oxidase sequence as described in SEQ ID 3 or a substantial equivalent thereof, the amino acid sequence contains at least one mutation selected from the group consisting of N25Y, T94A, D216N, R217C, M278T, Y329C, Q406R, Q406L, V492A, V494A, N521S, N535D, T549I, S567T, T578S and like mutations in subsantially equivalent sequences.

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2. An amino acid sequence according to claim 1, wherein the sequence is a mutant of a leucine dehydrogenase sequence as described in SEQ ID 2 or its substantial equivalent.

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3. An amino acid sequence according to claim 1, wherein the mutant is a mutant of a leucine dehydrogenase sequence as described in SEQ ID 2.

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4. An amino acid sequence according to claim 1, wherein the mutant is a mutant of a leucine dehydrogenase sequence that is at least 45% homologous to the sequence described in SEQ ID 2.

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- 5. An amino acid sequence according to claim 1, wherein the mutant is a mutant of a leucine dehydrogenase sequence that is at least 70% homologous to the sequence described in SEQ ID 2.
- 6. An amino acid sequence according to claim 1, wherein the mutant is a mutant of a leucine dehydrogenase sequence that is at least 80% homologous to the sequence described in SEQ ID 2.
- 7. An amino acid sequence according to claim 1, wherein the mutant is a mutant of a leucine dehydrogenase sequence that is at least 95% homologous to the sequence described in SEQ ID 2.
- 8. A deoxyribonucleic acid molecule containing a DNA sequence encoding the amino acid sequence of claim 2.
- 9. An amino acid sequence according to claim 1, wherein the sequence is a mutant of a formate dehydrogenase sequence as described in SEQ ID 1, or its substantial equivalent.
- 10. An amino acid sequence according to claim 1, wherein the mutant is a mutant of a formate dehydrogenase sequence as described in SEQ ID 1.
- of a formate dehydrogenase sequence that is at least 80% homologous to the sequence described in SEQ ID 1.
  - 12. An amino acid sequence according to claim 1, wherein the mutant is a mutant of a formate dehydrogenase sequence that is at least 95% homologous to the sequence described in SEQ ID 1.

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13. A deoxyribonucleic acid molecule containing a DNA sequence encoding the amino acid sequence of claim 9.

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14. An amino acid sequence according to claim 1, wherein the sequence is a mutant of a galactose oxidase sequence as described in SEQ ID 3, or its substantial equivalent.

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15. An amino acid sequence according to claim 1, wherein the mutant is a mutant of a galactose oxidase sequence as described in SEQ ID 3.

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16. An amino acid sequence according to claim 1, wherein the mutant is a mutant of a galactose oxidase sequence that is at least 80% homologous to the sequence described in SEQ ID 3.

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17. An amino acid sequence according to claim 1, wherein the mutant is a mutant of a galactose oxidase sequence that is at least 95% homologous to the sequence described in SEQ ID 3.

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19.

cofactor and an ammonia source.

18. A deoxyribonucleic acid molecule containing a DNA sequence encoding the amino acid sequence of claim 14.

ketoacid with the amino acid sequence of claim 2 in the presence of a reduced nicotinamide

A method for the production of an amino acid that comprises contacting a

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20. A method for the recycling of a nicotinamide cofactor that comprises contacting an oxidized nicotinamid cofactor with an amino acid sequence of claim 9 in the presence of a formate source.

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